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720 Supplemental information

Query sequence: AGYGSTQTAGEDSSLT	
BLAST against NCBI nr database 5000 hits	
٢	
Limit to sequences with identities ≥ 12	
1042 sequences	
Identify tandem array and classify repeats,	limit to sequences with continuous repeats ≥ 5
608 sequences	
<u> </u>	
Get BioProject ID	
300 unique BioProjects, 14 sequences with	n no BioProject ID
<u></u>	
Get Assembly ID for each BioProject	
All BioProjects had at least one assembly.	Checked up to the first 25 assemblies for each.
Get Assembly method for each Assembly I 67 sequences with no assembly method	D from eSummary
Limit assembly method to Oxford Nanopor	and/or PacBio /4 30 sequences from 9 projects with
170 sequences	A assembly method in SRA only
$\overline{\nabla}$	
Limit to unique sequences	
Final data set: 120 sequences + PbINP se	quence
ure S1. Flowchart and qua	ility control steps in sequence selection for bioinformatic analysis.
wn INPs from literature was	e used to generate a consensus sequence for WO_{-coils} which was then
within a month inclature wer	e used to generate a consensus sequence for wo-cons which was then

a data set using only genes from long-read DNA sequencing data.

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Figure S5. *E. coli* expressing INP mutant lacking R-coils shows no fibre clusters as observed in those cells overexpressing WT INP. **A-D**) Representative snapshots from 3-D cryo-tomograms showing cytoplasmic and extracellular features of various *E. coli* cells overexpressing an INP mutant in which all but the C-terminal R-coil have been replaced by WO-coils. All four images are in the same scale and the scale bar represents 100 nm.

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